

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Coleman, Timothy A
Rosen, Craig
- (ii) TITLE OF INVENTION: Endothelial-Monocyte Activating Polypeptide III
- (iii) NUMBER OF SEQUENCES: 7
- (iv) CORRESPONDENCE ADDRESS:
- (A) ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
CECCHI, STEWART & OLSTEIN
- (B) STREET: 6 BECKER FARM ROAD
- (C) CITY: ROSELAND
- (D) STATE: NEW JERSEY
- (E) COUNTRY: USA
- (F) ZIP: 07068
- (v) COMPUTER READABLE FORM:
- (A) MEDIUM TYPE: 3.5 INCH DISKETTE
- (B) COMPUTER: IBM PS/2
- (C) OPERATING SYSTEM: MS-DOS
- (D) SOFTWARE: WORD PERFECT 5.1
- (vi) CURRENT APPLICATION DATA:
- (A) APPLICATION NUMBER: 08/483,534
- (B) FILING DATE: 07 JUN 95
- (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
- (A) NAME: MULLINS, J.G.
- (B) REGISTRATION NUMBER: 33,073
- (C) REFERENCE/DOCKET NUMBER: 325800-464 (PF206)
- (ix) TELECOMMUNICATION INFORMATION:
- (A) TELEPHONE: 201-994-1700
- (B) TELEFAX: 201-994-1744

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS
- (A) LENGTH: 636 BASE PAIRS
- (B) TYPE: NUCLEIC ACID
- (C) STRANDEDNESS: SINGLE
- (D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TACCCCTGCC	CTGAAAAAAC	TGGCCAGCGC	TGCCTACCCA	GATCCCTCAA	AGCAGAAGCC	60
AATGGCCAAA	GGCCTGCCAA	GAATTAGAGAA	CCA GAG GAG	GTC ATC CCA TCC CGG		114
				Glu Glu Val Ile Pro Ser Arg		
			1	5		
CTG GAT ATC CGT	GTG GGG AAA ATC ATC ACT	GTG GAG AAG CAC CCA GAT				162
Leu Asp Ile Arg	Val Gly Lys Ile Ile Thr Val Glu Lys His Pro Asp					
10	15	20				
GCA GAC AGC CTG TAT GTA	GAG AAG ATT GAC GTG GGG GAA GCT GAA CCA					210
Ala Asp Ser Leu Tyr	Val Glu Lys Ile Asp Val Gly Glu Ala Glu Pro					
25	30	35				
CGG ACT GTG GTG AGC GGC	CTG GTA CAG TTC GTG CCC AAG GAG GAA CTG					258
Arg Thr Val Val Ser Gly	Leu Val Gln Phe Val Pro Lys Glu Glu Leu					
40	45	50	55			
CAG GAC AGG CTG GTA GTG	GTG CTG TGC AAC CTG AAA CCC CAG AAG ATG					306
Gln Asp Arg Leu Val Val	Leu Cys Asn Leu Lys Pro Gln Lys Met					
60	65	70				
AGA GGA GTC GAG TCC CAA GGC ATG CTT CTG TGT GCT TCT ATA GAA GGG						354
Arg Gly Val Glu Ser Gln Gly Met Leu Leu Cys Ala Ser Ile Glu Gly						
75	80	85				
ATA AAC CGC CAG GTT GAA CCT	CTG GAC CCT CCG GCA GGC TCT GCT CCT					402
Ile Asn Arg Gln Val Glu Pro	Ieu Asp Pro Pro Ala Gly Ser Ala Pro					
90	95	100				
GGT GAG CAC GTG TTT GTG AAG GGC	TAT GAA AAG GGC CAA CCA GAT GAG					450
Gly Glu His Val Phe Val Lys Gly Tyr Glu Lys Gly Gln Pro Asp Glu						
105	110	115				
GAG CTC AAG CCC AAG AAG AAA GTC TTC GAG AAG TTG CAG GCT GAC TTC						498
Glu Leu Lys Pro Lys Lys Val Phe Glu Lys Leu Gln Ala Asp Phe						
120	125	130	135			
AAA ATT TCT GAG GAG TGC ATC GCA CAG	TGG AAG CAA ACC AAC TTC ATG					546
Lys Ile Ser Glu Cys Ile Ala Gln Trp Lys Gln Thr Asn Phe Met						
140	145	150				
ACC AAG CTG GGC TCC ATT TCC TGT AAA TCG CTG AAA GGG GGG AAC ATT						594
Thr Lys Leu Gly Ser Ile Ser Cys Lys Ser Leu Lys Gly Gly Asn Ile						
155	160	165				
AGC TAG CCAGCCCAGC ATCTTCCCCC CTTCTTCCAC CACTGA						636
Ser						

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS
 - (A) LENGTH: 168 AMINO ACIDS
 - (B) TYPE: AMINO ACID
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: LINEAR

- (ii) MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Glu Glu Val Ile Pro Ser Arg Leu Asp Ile Arg Val Gly Lys Ile Ile
5 10 15

Thr Val Glu Lys His Pro Asp Ala Asp Ser Leu Tyr Val Glu Lys Ile
20 25 30

Asp Val Gly Glu Ala Glu Pro Arg Thr Val Val Ser Gly Leu Val Gln
35 40 45

Phe Val Pro Lys Glu Glu Leu Gln Asp Arg Leu Val Val Val Leu Cys
50 55 60

Asn Leu Lys Pro Gln Lys Met Arg Gly Val Glu Ser Gln Gly Met Leu
65 70 75 80

Leu Cys Ala Ser Ile Glu Gly Ile Asn Arg Gln Val Glu Pro Leu Asp
85 90 95

Pro Pro Ala Gly Ser Ala Pro Gly Glu His Val Phe Val Lys Gly Tyr
100 105 110

Glu Lys Gly Gln Pro Asp Glu Glu Leu Lys Pro Lys Lys Val Phe
115 120 125

Glu Lys Leu Gln Ala Asp Phe Lys Ile Ser Glu Glu Cys Ile Ala Gln
130 135 140

Trp Lys Gln Thr Asn Phe Met Thr Lys Leu Gly Ser Ile Ser Cys Lys
145 150 155 160

Ser Leu Lys Gly Gly Asn Ile Ser
165

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 28 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR

(ii) MOLECULE TYPE: Oligonucleotide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GATCGGATCC GAGGAGGTCA TCCCATCC

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(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 28 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: Oligonucleotide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GATCAAGCTT CTAGATAATG TTCCCCCC

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(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 28 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: Oligonucleotide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GATCGGATCC GAGGAGGTCA TCCCCATCC

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(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 28 BASE PAIRS
(B) TYPE: NUCLEIC ACID
(C) STRANDEDNESS: SINGLE
(D) TOPOLOGY: LINEAR
- (ii) MOLECULE TYPE: Oligonucleotide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GATCAAGCTT CTAGATAATG TTCCCCCC

28

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS
(A) LENGTH: 183 AMINO ACIDS
(B) TYPE: AMINO ACID
(C) STRANDEDNESS:
(D) TOPOLOGY: LINEAR

(ii)

MOLECULE TYPE: PROTEIN

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Lys Gly Glu Lys Lys Glu Lys Lys Gln Gln Ser Ile Ala Gly Ser
5 10 15
Ala Asp Ser Lys Pro Ile Asp Val Ser Arg Leu Asp Leu Arg Ile
20 25 30
Gly Cys Ile Ile Thr Ala Arg Lys His Pro Asp Ala Asp Ser Leu
35 40 45
Tyr Val Glu Glu Val Asp Val Gly Glu Ile Ala Pro Arg Thr Val
50 55 60
Val Ser Gly Leu Val Asn His Val Pro Leu Glu Gln Met Gln Asn
65 70 75
Arg Met Val Ile Leu Leu Cys Asn Leu Lys Pro Ala Lys Met Arg
80 85 90
Gly Val Lys Ser Gln Ala Met Val Met Cys Ala Ser Ser Pro Glu
95 100 105
Lys Ile Glu Ile Leu Ala Pro Pro Asn Gly Ser Val Pro Gly Asp
110 115 120
Arg Ile Thr Phe Asp Ala Phe Pro Gly Glu Pro Asp Lys Glu Lys
125 130 135
Asn Pro Lys Lys Lys Ile Trp Glu Gln Ile Gln Pro Asp Leu His
140 145 150
Thr Asn Asp Glu Cys Val Ala Thr Tyr Lys Glu Val Pro Phe Glu
155 160 165
Val Lys Gly Lys Gly Val Cys Arg Ala Gln Thr Met Ser Asn Ser
170 175 180
Gly Ile Lys

SEQUENCE ID NO: 7